REMARKS

These remarks are in response to the Final Office Action mailed April 28, 2004. The specification has been amended to remove hyperlink and/or other forms of browser-executable code. Claim 9 has been amended. The amendments to the claims are supported in claim 9 as presently pending. In addition, support for the amendments can be found in Example 2 (beginning at page 76); page 89, line 30 to page 90, line 31; and Figure 14 and 15. No new matter is believed to have been introduced.

I. REJECTION UNDER 35 U.S.C. §112, SECOND PARAGRAPH

Claims 9-11 stand rejected under 35 U.S.C. §112, second paragraph as allegedly being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 9 (upon which claims 10 and 11 depend) has been amended to more clearly set forth the method recited. The amendments to claim 9 have, in one aspect, merely separated various elements of the process for ease of reading. The underlying "cubic lattice" and the "force field" are "virtual" representations as inherent in a computer implemented method. The term, "knowledge based origin is defined by the method of the claim (e.g., "apply secondary constraints and/or tertiary constraints to a subset of, or all of, the interaction centers of the interaction center chain to generate a knowledge based origin defined by a virtual force field of short-range interactions"). Applicants believe that the foregoing amendments and the present remarks overcome the rejection. Accordingly, Applicants respectfully request withdrawal of the §112, second paragraph rejection.

II. REJECTION UNDER 35 U.S.C. §102

Claims 9-11 stand rejected under 35 U.S.C. §102 as allegedly anticipated by Kolinski et al. #1 ("Workshop") and as anticipated by Kolinski et al. #2 (J. Phys. Chem). Applicants respectfully traverse these rejections.

Applicants respectfully aver that Kolinski, HRCL Workshop does not describe a computer-assisted method for determining a three-dimensional structure of a target amino acid sequence by aligning a target amino acid sequence with a template amino acid sequence and producing from the alignment a three dimensional reduced protein model comprising representations of side chains of amino acid residues comprising a target protein, wherein said representations of side chains of amino acid residues are converted to interaction centers and each interaction center comprises a pseudoatom representing a center of mass of the side chain of the represented amino acid to which the interaction center corresponds, and each interaction center is connected to an immediately proximal interaction center and an immediately distal interaction center via a virtual covalent bond to produce an interaction center chain, which is projected onto an underlying cubic lattice to produce a projected chain of interaction centers, and then secondary constraints and/or tertiary constraints are applied to a subset of, or all of, the interaction centers of the interaction center chain to generate a force field comprising short-range interactions, thereby producing a data set representing a three-dimensional model structure of the target protein.

The computer implemented methods of the instant invention use a force field designed entirely of a "knowledge-based" origin. It is noted that some terms, such as the generic short- and long-range potentials, provide a bias toward protein-like short- and long-range correlations (see page 41, lines 29 to 31 of the specification). It is noted that the force used in the methods of the invention approximately reproduce the main features of globular proteins, and does so in a different geometrical context, namely, using pseudoatoms representing side chain centers of mass. Moreover, the instant invention is based on a less complex representation and simpler definition of the force field, and is more computationally efficient than C-alpha-based models, such as MONSSTER (see page 43, lines 1 to 11, of the specification).

Kolinski, HRCL Workshop does not produce an interaction center chain and project the interaction center chain onto an underlying cubic lattice to produce a projected chain of interaction centers by using a calculated force field comprising short-range interactions as set forth in the specification, as discussed above. Accordingly, because Kolinski, HRCL Workshop

is not a single prior source that contains each and every limitation of the claimed invention this rejection 35 U.S.C. 102(a) can be withdrawn.

The Patent Office also alleges that Kolinski, J. Phys. Chem. anticipates Applicants' claims 9-11. Applicants respectfully traverse this rejection.

The Patent Office alleges that Kolinski, J. Phys. Chem. teaches the idea of side chain representation into computer modeling techniques for protein structure, and that the lattice chains of centers of mass of side chains is employed which utilizes Monte Carlo simulation to represent the three-dimensional structure of a target polypeptide.

Applicants respectfully aver that Kolinski, J. Phys. Chem. does not describe a computer-assisted method for determining a three-dimensional structure of a target amino acid sequence by aligning a target amino acid sequence with a template amino acid sequence and producing from the alignment a three dimensional reduced protein model comprising representations of side chains of amino acid residues comprising a target protein, wherein said representations of side chains of amino acid residues are converted to interaction centers and each interaction center comprises a pseudoatom representing a center of mass of the side chain of the represented amino acid to which the interaction center corresponds, and each interaction center is connected to an immediately proximal interaction center and an immediately distal interaction center via a virtual covalent bond to produce an interaction center chain, which is projected onto an underlying cubic lattice to produce a projected chain of interaction centers, and then secondary constraints and/or tertiary constraints are applied to a subset of, or all of, the interaction centers of the interaction center chain to generate a force field comprising short-range interactions, thereby producing a data set representing a three-dimensional model structure of the target protein.

In contrast, the Kolinski, J. Phys. Chem. model employs atom representation of amino acid residues, centered on protein side groups. Characteristic short-range distance correlations have been built into the model, thereby providing a rather accurate description of protein-like conformational stiffness. Sequence-specific interaction schemes have been derived from sequence similarity and sequence-structure compatibility studies (see abstract). The Kolinski, J. Phys. Chem. model "employ[s] only the homology ... of small fragments of protein sequences,

thereby allowing for the construction of a potential for sequences having no globally homologous counterparts in the structural database." (see page 4628, right-hand column, last sentence first full paragraph); and, "[t]he purpose of this work is to analyze the role of the generic protein-like regularities seen in protein chains, the role of sequence-specific short-range correlations of the side chain positions, and this interplay." (see the sentence spanning pages 4628 and 4629).

Kolinski, J. Phys. Chem. does not produce an interaction center chain and project the interaction center chain onto an underlying cubic lattice to produce a projected chain of interaction centers by using a calculated force field comprising short-range interactions. Accordingly, because Kolinski, J. Phys. Chem. is not a single prior source that contains each and every limitation of the claimed invention this rejection 35 U.S.C. 102(a) can be withdrawn.

Enclosed is a $490 check for the Petition for Extension of Time fee. Please apply any other charges or credits to deposit account 06-1050.

Respectfully submitted,

Date: 10/28/04

Joseph R. Baker, Jr.
Reg. No. 40,900

Fish & Richardson P.C.
PTO Customer No. 20985
12390 El Camino Real
San Diego, California 92130
Telephone: (858) 678-5070
Facsimile: (858) 678-5099